

0590
1009

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/940,063

DATE: 10/01/2001

TIME: 13:58:13

Input Set : N:\Crif3\RULE60\09940063.txt

Output Set: N:\CRF3\10012001\I940063.raw

#2

4 <110> APPLICANT: Briskin, Michael J.
5 Murphy, Kristine E.
6 Wilbanks, Alyson M.
7 Wu, Lijun
9 <120> TITLE OF INVENTION: Novel Antibodies and Ligands for "Bonzo"
10 Chemokine Receptor
12 <130> FILE REFERENCE: 1855.1070-000
14 <140> CURRENT APPLICATION NUMBER: 09/940,063
15 <141> CURRENT FILING DATE: 2001-08-27
17 <150> PRIOR APPLICATION NUMBER: 09/449,437
18 <151> PRIOR FILING DATE: 1999-11-24
20 <160> NUMBER OF SEQ ID NOS: 18
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1029
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <400> SEQUENCE: 1

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31 gaggagcattc aagacttcct gcagttcagc aagggtcttc tgccctgcat gtacctggtg 120
32 gtgtttgtct gtggtctggt ggggaactct ctggtgctgg tcatatccat cttctaccat 180
33 aagttgcaga gcctgacgga tgtgttcctg gtgaacctac ccctggctga cctggtgttt 240
34 gtctgcactc tgcccttctg ggcctatgca ggcattccat aatgggtgtt tggccagggtc 300
35 atgtgcaaga gcctactggg catctacact attaacttct acacgtccat gctcatcctc 360
36 acctgcatca ctgtggatcg ttctattgta gtggttaagg ccaccaaggc ctacaaccag 420
37 caagccaaga ggatgacctg gggcaagggt accagcttgc tcatctgggt gatatccctg 480
38 ctgggttctc tgccccaat tatctatggc aatgtcttta atctcgacaa gctcatatgt 540
39 gggttaccatg acgaggcaat ttccactgtg gttcttgcca cccagatgac actgggggttc 600
40 ttcttgccac tgctcaccat gattgtctgc tattcagtca taatcaaaac actgcttcat 660
41 gctggaggct tccagaagca cagatctcta aagatcatct tcctgggtgat ggctgtgttc 720
42 ctgctgaccc agatgccctt caacctcatg aagttcatcc gcagcacaca ctgggaatac 780
43 tatgccatga ccagctttca ctacaccatc atggtgacag aggccatcgc atacctgagg 840
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45 aaacttgtga aggacattgg ttgcctccct taccttgggg tctcacatca atggaaatct 960
46 tctgaggaca attccaagac tttttctgcc tcccacaatg tggaggccac cagcatgttc 1020
47 cagttatag 1029

49 <210> SEQ ID NO: 2
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51 <212> TYPE: PRT
52 <213> ORGANISM: Homo sapiens
54 <400> SEQUENCE: 2

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57 Asp Ser Ser Gln Glu Glu His Gln Asp Phe Leu Gln Phe Ser Lys Val
58 20 25 30
59 Phe Leu Pro Cys Met Tyr Leu Val Val Phe Val Cys Gly Leu Val Gly
60 35 40 45

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61 Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser
62      50                      55                      60
63 Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe
64 65                      70                      75                      80
65 Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val
66                      85                      90                      95
67 Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn
68                      100                     105                     110
69 Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe
70                      115                     120                     125
71 Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg
72                      130                     135                     140
73 Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu
74 145                     150                     155                     160
75 Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp
76                      165                     170                     175
77 Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu
78                      180                     185                     190
79 Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile
80                      195                     200                     205
81 Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe
82                      210                     215                     220
83 Gln Lys His Arg Ser Leu Lys Ile Ile Phe Leu Val Met Ala Val Phe
84 225                     230                     235                     240
85 Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr
86                      245                     250                     255
87 His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val
88                      260                     265                     270
89 Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr
90                      275                     280                     285
91 Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys
92                      290                     295                     300
93 Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser
94 305                     310                     315                     320
95 Ser Glu Asp Asn Ser Lys Thr Phe Ser Ala Ser His Asn Val Glu Ala
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98                      340
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108 ttctgctcct gctggtgtac ctgactcagc caggcaatgg caacgagggc agcgtcactg 120
109 gaagttgtta ttgtggtaaa agaatttctt ccgactcccc gccatcgggt cagttcatga 180
110 atcgtctccg gaaacacctg agagcttacc atcgggtgtct atactacacg aggttccagc 240
111 tcctttcctg gagcgtgtgt ggaggcaaca aggacccatg ggttcaggaa ttgatgagct 300
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114 cccctgccca gatgctcctg tccaccttgc agtccactca gcgccccacc ctcccagtag 480
115 gatcactgtc ctoggacaaa gagctcactc gtcccaatga aaccaccatt cacactgcgg 540
116 gccacagtct ggcagttggg cctgaggctg gggagaacca gaagcagccg gaaaaaaatg 600
117 ctggtcccac agccaggaca tcagccacag tgccggctct gtgcctcctg gccatcatct 660
118 tcactctcac cgcagccctt tctatgtgct tgtgcaagag gaggaggggg cagtcaccgc 720
119 agtctctctc agatctgccg gttcattata tacctgtggc acctgactct aatacctgag 780
120 ccaagaatgg aagcttgtga ggagacggac tctatgttgc ccaggctgtt atggaactcc 840
121 tgagtcaagt gatcctccca ccttggcctc tgaagggtgc aggattatag gcgtcaccta 900
122 ccacatccag cctacacgta tttgttaata tctaacatag gactaaccag ccactgccct 960
123 ctcttagggc cctcatttaa aaacggttat actataaaat ctgcttttca cactgggtga 1020
124 taataacttg gacaaattct atgtgtatgt tgttttgttt tgctttgctt tgttttgaga 1080
125 cggagtctcg ctctgtcctc caggctggag tgcagtggca tgatctcggc tcaactgcaac 1140
126 ccccatctcc caggttcaag cgattctcct gcctcctcct gagtagctgg gactacaggt 1200
127 gctcaccacc acaccggct aattttttgt attttttagta gagaccgggg ttccaccatg 1260
128 ttgaccaggc tggctctgaa ctctgacct ggtgatctgc ccaccaggc ctcccaaagt 1320
129 gctgggatta aaggtgtgag ccaccatgcc tggccctatg tgtgtttttt aactactaaa 1380
130 aattattttt gtaatgattg agtctcttt atggaacaa ctggcctcag cccttgccgc 1440
131 ctactgtga ttcttggtt cattttttgc tgatggttcc cctcgtccc aaatctctct 1500
132 ccagtacac cagttgttcc tccccacct cagccctctc ctgcactctc ctgtaccgc 1560
133 aacgaaggcc tgggttttcc caccctccct ccttagcagg tgcctgtctg ggacaccata 1620
134 cgggttggtt tcacctctc agtcccttgc ctaccocagt gagagtctga tcttgttttt 1680
135 attgttattg cttttattat tattgtttt attatcatta aaactctagt tcttgttttg 1740
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140 <212> TYPE: PRT

141 <213> ORGANISM: Homo sapiens

143 <400> SEQUENCE: 4

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146 Leu Leu Leu Leu Val Tyr Leu Thr Gln Pro Gly Asn Gly Asn Glu Gly
147 20 25 30
148 Ser Val Thr Gly Ser Cys Tyr Cys Gly Lys Arg Ile Ser Ser Asp Ser
149 35 40 45
150 Pro Pro Ser Val Gln Phe Met Asn Arg Leu Arg Lys His Leu Arg Ala
151 50 55 60
152 Tyr His Arg Cys Leu Tyr Tyr Thr Arg Phe Gln Leu Leu Ser Trp Ser
153 65 70 75 80
154 Val Cys Gly Gly Asn Lys Asp Pro Trp Val Gln Glu Leu Met Ser Cys
155 85 90 95
156 Leu Asp Leu Lys Glu Cys Gly His Ala Tyr Ser Gly Ile Val Ala His
157 100 105 110
158 Gln Lys His Leu Leu Pro Thr Ser Pro Pro Ile Ser Gln Ala Ser Glu
159 115 120 125
160 Gly Ala Ser Ser Asp Ile His Thr Pro Ala Gln Met Leu Leu Ser Thr
161 130 135 140
162 Leu Gln Ser Thr Gln Arg Pro Thr Leu Pro Val Gly Ser Leu Ser Ser
163 145 150 155 160

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166 His Ser Leu Ala Val Gly Pro Glu Ala Gly Glu Asn Gln Lys Gln Pro
167                               180                               185                               190
168 Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr Val Pro Val
169                               195                               200                               205
170 Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala Pro Ser Tyr
171                               210                               215                               220
172 Val Leu Cys Lys Arg Arg Arg Gly Gln Ser Pro Gln Ser Ser Pro Asp
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186 cctcacaggt cggcgacgg gccaggcggg cggcctcctg aaccgaaccg aatcggtcc 180
187 tcgggcgctc gtctctccgc cctcctcgc ccgcgcggc agttttcttt cggtttcttc 240
188 caagattcct ggccttccct cgaaggagcc gggccagtg cgggggcgca gggcgcgga 300
189 gctccacctc ctcggttttc cctgcgtcca gaggtggca tggcgcgggc cgagtactga 360
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192 gagcatgtct gggagtcaga gcgaggtggc tccatccccg cagagtcgcg ggagccccga 540
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197 cgtgtgtgga ggcaacaagg acctatgggt tcaggaattg atgagctgtc ttgatctcaa 840
198 agaattgtga catgcttact cggggattgt ggcccaccag aagcatttac ttctaccag 900
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217 tggcttcatt ttttgctgat gggtcccccct cgtcccaaat ctctctccca gtacaccagt 2040
218 tgttcctccc ccacctcagc cctctcctgc atcctcctgt acccgcaacg aaggcctggg 2100
219 ctttcccacc ctccctcctt agcagggtgcc gtgctgggac accatacggg ttggtttcac 2160
220 ctccctcagtc ccttgcttac cccagtgaga gtctgatctt gtttttattg ttattgcttt 2220
221 tattattatt gcttttatta tcattaaaac tctagttctt gttttgtctc tcaaaaaaaaa 2280
222 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2309
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225 <211> LENGTH: 254
226 <212> TYPE: PRT
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229 <400> SEQUENCE: 6
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233 20 25 30
234 Ser Val Thr Gly Ser Cys Tyr Cys Gly Lys Arg Ile Ser Ser Asp Ser
235 35 40 45
236 Pro Pro Ser Val Gln Phe Met Asn Arg Leu Arg Lys His Leu Arg Ala
237 50 55 60
238 Tyr His Arg Cys Leu Tyr Tyr Thr Arg Phe Gln Leu Leu Ser Trp Ser
239 65 70 75 80
240 Val Cys Gly Gly Asn Lys Asp Pro Trp Val Gln Glu Leu Met Ser Cys
241 85 90 95
242 Leu Asp Leu Lys Glu Cys Gly His Ala Tyr Ser Gly Ile Val Ala His
243 100 105 110
244 Gln Lys His Leu Leu Pro Thr Ser Pro Pro Thr Ser Gln Ala Ser Glu
245 115 120 125
246 Gly Ala Ser Ser Asp Ile His Thr Pro Ala Gln Met Leu Leu Ser Thr
247 130 135 140
248 Leu Gln Ser Thr Gln Arg Pro Thr Leu Pro Val Gly Ser Leu Ser Ser
249 145 150 155 160
250 Asp Lys Glu Leu Thr Arg Pro Asn Glu Thr Thr Ile His Thr Ala Gly
251 165 170 175
252 His Ser Leu Ala Val Gly Pro Glu Ala Gly Glu Asn Gln Lys Gln Pro
253 180 185 190
254 Glu Lys Asn Ala Gly Pro Thr Ala Arg Thr Ser Ala Thr Val Pro Val
255 195 200 205
256 Leu Cys Leu Leu Ala Ile Ile Phe Ile Leu Thr Ala Ala Leu Ser Tyr
257 210 215 220
258 Val Leu Cys Lys Arg Arg Arg Gly Gln Ser Pro Gln Ser Ser Pro Asp
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261 245 250
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267 <213> ORGANISM: Homo sapiens
269 <400> SEQUENCE: 7

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VERIFICATION SUMMARY

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